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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/923,444A

DATE: 02/06/2002
 TIME: 08:56:41

Input Set : N:\Crf3\RULE60\09923444A.txt
 Output Set: N:\CRF3\02062002\I923444A.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
 6 (i) APPLICANT: LI, YI
 7 FLEISCHMANN, ROBERT
 9 (ii) TITLE OF INVENTION: NEUROTRANSMITTER TRANSPORTER
 11 (iii) NUMBER OF SEQUENCES: 6
 13 (iv) CORRESPONDENCE ADDRESS:
 14 (A) ADDRESSEE: Human Genome Sciences, Inc.
 15 (B) STREET: 9410 Key West Avenue
 16 (C) CITY: Rockville
 17 (D) STATE: MD
 18 (E) COUNTRY: US
 19 (F) ZIP: 20850
 21 (v) COMPUTER READABLE FORM:
 22 (A) MEDIUM TYPE: Floppy disk
 23 (B) COMPUTER: IBM PC compatible
 24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 27 (vi) CURRENT APPLICATION DATA:
 C--> 28 (A) APPLICATION NUMBER: US/09/923,444A
 C--> 29 (B) FILING DATE: 08-Aug-2001
 30 (C) CLASSIFICATION:
 32 (vii) PRIOR APPLICATION DATA:
 33 (A) APPLICATION NUMBER: 09/062,815
 34 (B) FILING DATE: 199-12-20
 36 (viii) ATTORNEY/AGENT INFORMATION:
 37 (A) NAME: Michele M. Wales
 38 (B) REGISTRATION NUMBER: 43,975
 39 (C) REFERENCE/DOCKET NUMBER: PF116
 41 (ix) TELECOMMUNICATION INFORMATION:
 42 (A) TELEPHONE: (301) 309-8504
 43 (B) TELEFAX: (301) 309-8439
 46 (2) INFORMATION FOR SEQ ID NO: 1:
 48 (i) SEQUENCE CHARACTERISTICS:
 49 (A) LENGTH: 2485 base pairs
 50 (B) TYPE: nucleic acid
 51 (C) STRANDEDNESS: single
 52 (D) TOPOLOGY: linear
 54 (ii) MOLECULE TYPE: DNA (genomic)
 57 (ix) FEATURE:
 58 (A) NAME/KEY: CDS
 59 (B) LOCATION: 266..2446
 62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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64	CGGAGGCAGG	GAGTGAGGAG	CGAGCGGAGT	CGCGTGC GCC	GGCGCGAGCT	CCGGGTCGCC	60
66	CCAGCCCCAG	CCGGGGGCCT	GTGGCGGGGG	AGGAGCTGTG	CGTCCGCGAC	CCGTCCGGGAT	120
68	CGCAGCTGCT	CGGCCGGAGT	GCACGGGCGG	AGTCTGCGCG	ACTACCCACG	CGTGACAGGT	180
70	CCCTGAATGA	GAAGGAGCTG	ACAGCAGCTG	AATTCCATCT	TCTCTGTGTG	CTGGGGAGCA	240
72	GGGCTACACG	GCCCAGGTGG	CATCA ATG	CCG AAG AAC	AGC AAA GTG	ACC CAG	292
73			Met	Pro	Lys	Asn Ser Lys Val Thr Gln	
74			1		5		
76	CGT GAG CAC	AGC AGT GAG	CAT GTC	ACT GAG	TCC GTG	GCC GAC CTG CTG	340
77	Arg Glu His	Ser Ser Glu	His Val Thr	Glu Ser Val	Ala Asp Leu	Leu	
78	10		15		20	25	
80	GCC CTC GAG	GAG CCT GTG	GAC TAT AAG	CAG AGT GTA	CTG AAT GTG	GCT	388
81	Ala Leu Glu	Glu Pro Val	Asp Tyr Lys	Gln Ser Val	Leu Asn Val	Ala	
82		30		35		40	
84	GGT GAG GCA	GGC GGC AAG	CAG AAG GCG	GTG GAG GAG	GAG CTG GAT	GCA	436
85	Gly Glu Ala	Gly Gly Lys	Gln Lys Ala	Val Glu Glu	Glu Leu Asp	Ala	
86		45		50		55	
88	GAG GAC CGG	CCG GCC TGG	AAC AGT AAG	CTG CAG TAC	ATC CTG GCC	CAG	484
89	Glu Asp Arg	Pro Ala Trp	Asn Ser Lys	Leu Gln Tyr	Ile Leu Ala	Gln	
90		60		65		70	
92	ATT GGC TTC	TCT GTG GGC	CTC GGC AAC	ATC TGG AGG	TTC CCC TAC	CTG	532
93	Ile Gly Phe	Ser Val Gly	Leu Gly Asn	Ile Trp Arg	Phe Pro Tyr	Leu	
94		75		80		85	
96	TGC CAG AAA	AAT GGA GGA	GGT GCT TAC	CTG GTG CCC	TAC CTG GTG	CTG	580
97	Cys Gln Lys	Asn Gly Gly	Gly Ala Tyr	Leu Val Pro	Tyr Leu Val	Leu	
98	90		95		100	105	
100	CTG ATC ATC	ATC GGG ATC	CCC CTC TTC	TTC CTG GAG	CTG GCT GTG	GGT	628
101	Leu Ile Ile	Ile Gly Ile	Pro Leu Phe	Phe Leu Glu	Leu Ala Val	Gly	
102		110		115		120	
104	CAG AGG ATC	CGC CGC GGA	AGC ATC GGT	GTG TGG CAC	TAT ATA TGT	CCC	676
105	Gln Arg Ile	Arg Arg Gly	Ser Ile Gly	Val Trp His	Tyr Ile Cys	Pro	
106		125		130		135	
108	CGC CTG GGG	GGG ATC GGC	TTC TCC AGC	TGC ATA GTC	TGT CTC TTT	GTG	724
109	Arg Leu Gly	Gly Ile Gly	Phe Ser Cys	Ile Val Cys	Leu Phe Val		
110		140		145		150	
112	GGG CTG TAT	TAT AAT GTG	ATC ATC GGG	TGG AGC ATC	TTC TAT TTC	TTC	772
113	Gly Leu Tyr	Tyr Tyr Asn	Val Ile Ile	Gly Trp Ser	Ile Phe Tyr	Phe Phe	
114		155		160		165	
116	AAG TCC TTC	CAG TAC CCG	CTG CCC TGG	AGT GAA TGT	CCT GTC GTC	AGG	820
117	Lys Ser Phe	Gln Tyr Pro	Leu Pro Trp	Ser Glu Cys	Pro Val Val	Arg	
118	170		175		180	185	
120	AAT GGG AGC	GTC GCA GTG	GTG GAG GCA	GAG TGT GAA	AAG AGC TCA	GCC	868
121	Asn Gly Ser	Val Ala Val	Val Glu Ala	Glu Cys Glu	Lys Ser Ser	Ala	
122		190		195		200	
124	ACT ACC TAC	TTC TGG TAC	CGA GAG GCT	TTG GAC ATC	TCT GAC TCC	ATC	916
125	Thr Thr Tyr	Phe Trp Tyr	Arg Glu Ala	Leu Asp Ile	Ser Asp Ser	Ile	
126		205		210		215	
128	TCG GAG AGT	GGG GGC CTC	AAC TGG AAG	ATG ACC CTG	TGC CTC CTC	GTG	964
129	Ser Glu Ser	Gly Gly Leu	Asn Trp Lys	Met Thr Leu	Cys Leu Leu	Val	
130		220		225		230	

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132	GTC	TGG	AGC	ATC	GGG	GGG	ATG	GCT	GTC	GGT	AAG	GGC	ATC	CAG	TCC	TCG	1012
133	Val	Trp	Ser	Ile	Gly	Gly	Met	Ala	Val	Gly	Lys	Gly	Ile	Gln	Ser	Ser	
134	235						240					245					
136	GGG	AAG	GTG	ATG	TAT	TTC	AGC	TCC	CTC	TTC	CCC	TAC	GTG	GTG	CTG	GCC	1060
137	Gly	Lys	Val	Met	Tyr	Phe	Ser	Ser	Leu	Phe	Pro	Tyr	Val	Val	Leu	Ala	
138	250					255					260					265	
140	TGC	TTC	CTG	GTC	CGG	GGG	TTG	TTG	TTG	CGA	GGG	GCA	GTT	GAT	GGC	ATC	1108
141	Cys	Phe	Leu	Val	Arg	Gly	Leu	Leu	Leu	Arg	Gly	Ala	Val	Asp	Gly	Ile	
142					270					275						280	
144	CTA	CAC	ATG	TTC	ACT	CCC	AAG	CTG	GTC	AAG	ATG	CTG	GAC	CCC	CAG	GTG	1156
145	Leu	His	Met	Phe	Thr	Pro	Lys	Leu	Val	Lys	Met	Leu	Asp	Pro	Gln	Val	
146					285					290						295	
148	TGG	CGG	GAG	GTA	GCT	ACC	CAG	GTC	TTC	TTT	GGC	TTG	GGT	CTG	GGC	TTT	1204
149	Trp	Arg	Glu	Val	Ala	Thr	Gln	Val	Phe	Phe	Gly	Leu	Gly	Leu	Gly	Phe	
150					300					305						310	
152	GGT	GGT	GTC	ATT	GTC	TTC	TCC	AGT	TAC	AAT	AAG	CAG	GAC	AAC	AAC	TGC	1252
153	Gly	Gly	Val	Ile	Val	Phe	Ser	Ser	Tyr	Asn	Lys	Gln	Asp	Asn	Asn	Cys	
154		315					320					325					
156	CAC	TTC	GAT	GGC	GCC	CTG	GTG	TCC	TTC	ATC	AAC	TTC	TTC	ACG	TCA	GTG	1300
157	His	Phe	Asp	Gly	Ala	Leu	Val	Ser	Phe	Ile	Asn	Phe	Phe	Thr	Ser	Val	
158	330					335					340					345	
160	TTG	GCC	ACC	CTC	GTG	GTG	TTT	GTT	GTT	TTG	GGC	TTC	AAG	GCC	AAC	ATC	1348
161	Leu	Ala	Thr	Leu	Val	Val	Phe	Val	Val	Leu	Gly	Phe	Lys	Ala	Asn	Ile	
162					350					355						360	
164	ATG	AAT	GAG	AAG	TGT	GTG	GTC	GAG	AAT	GCT	GAG	AAA	ATC	CTA	GGG	TAC	1396
165	Met	Asn	Glu	Lys	Cys	Val	Val	Glu	Asn	Ala	Glu	Lys	Ile	Leu	Gly	Tyr	
166					365					370						375	
168	CTT	AAC	ACC	AAC	GTC	CTG	AGC	CGG	GAC	CTC	ATC	CCA	CCC	CAC	GTC	AAC	1444
169	Leu	Asn	Thr	Asn	Val	Leu	Ser	Arg	Asp	Leu	Ile	Pro	Pro	His	Val	Asn	
170					380					385						390	
172	TTC	TCC	CAC	CTG	ACC	ACA	AAG	GAC	TAC	ATG	GAG	ATG	GAC	AAT	GTC	ATC	1492
173	Phe	Ser	His	Leu	Thr	Thr	Lys	Asp	Tyr	Met	Glu	Met	Asp	Asn	Val	Ile	
174							400									405	
176	ATG	ACC	GTG	AAG	GAG	GAC	CAG	TTC	TCA	GCC	CTG	GGC	CTT	GAC	CCC	TGC	1540
177	Met	Thr	Val	Lys	Glu	Asp	Gln	Phe	Ser	Ala	Leu	Gly	Leu	Asp	Pro	Cys	
178	410					415					420					425	
180	CTT	CTG	GAG	GAC	GAG	CTG	GAC	AAG	TCC	GTG	CAG	GGC	ACA	GGC	CTG	GCC	1588
181	Leu	Leu	Glu	Asp	Glu	Leu	Asp	Lys	Ser	Val	Gln	Gly	Thr	Gly	Leu	Ala	
182					430					435						440	
184	TTC	ATC	GCC	TTC	ACT	GAG	GCC	ATG	ACG	CAC	TTC	CCC	ACC	TCC	CCG	TTC	1636
185	Phe	Ile	Ala	Phe	Thr	Glu	Ala	Met	Thr	His	Phe	Pro	Thr	Ser	Pro	Phe	
186					445					450						455	
188	TGG	TCC	GTC	ATG	TTC	TTC	TTG	ATG	CTT	ATC	AAC	CTG	GGC	CTG	GGC	AGC	1684
189	Trp	Ser	Val	Met	Phe	Phe	Leu	Met	Leu	Ile	Asn	Leu	Gly	Leu	Gly	Ser	
190					460					465						470	
192	ATG	ATC	GGG	ACC	ATG	GCA	GGC	ATC	ACC	ACG	CCC	ATC	ATC	GAC	ACC	TCC	1732
193	Met	Ile	Gly	Thr	Met	Ala	Gly	Ile	Thr	Thr	Pro	Ile	Ile	Asp	Thr	Ser	
194					475					480						485	
196	AAG	GTG	CCC	AAG	GAG	ATG	TTC	ACA	GTG	GGC	TGC	TGT	GTC	TTT	ACA	TTC	1780

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197	Lys	Val	Pro	Lys	Glu	Met	Phe	Thr	Val	Gly	Cys	Cys	Val	Phe	Thr	Phe	
198	490					495					500					505	
200	CTC	GTG	GGA	CTG	TTG	TTC	GTC	CAG	CGC	TCC	GGA	AAC	TAC	TTT	GTC	ACC	1828
201	Leu	Val	Gly	Leu	Leu	Phe	Val	Gln	Arg	Ser	Gly	Asn	Tyr	Phe	Val	Thr	
202					510					515					520		
204	ATG	TTC	GAT	GAC	TAC	TCA	GCC	ACG	CTG	CCA	CTC	ACT	CTC	ATC	GTC	ATC	1876
205	Met	Phe	Asp	Asp	Tyr	Ser	Ala	Thr	Leu	Pro	Leu	Thr	Leu	Ile	Val	Ile	
206				525					530					535			
208	CTT	GAG	AAC	ATC	GCT	GTG	GCC	TGG	ATT	TAT	GGA	CCC	AAG	AAG	TTC	ATG	1924
209	Leu	Glu	Asn	Ile	Ala	Val	Ala	Trp	Ile	Tyr	Gly	Pro	Lys	Lys	Phe	Met	
210			540					545					550				
212	CAG	GAG	CTG	ACG	GAG	ATG	CTG	GGC	TTC	CGC	CCC	TAC	CGC	TTC	TAT	TTC	1972
213	Gln	Glu	Leu	Thr	Glu	Met	Leu	Gly	Phe	Arg	Pro	Tyr	Arg	Phe	Tyr	Phe	
214		555					560				565						
216	TAC	ATG	TGG	AAG	TTC	GTG	TCT	CCA	CTA	TGC	ATG	GCT	GTG	CTC	ACC	ACA	2020
217	Tyr	Met	Trp	Lys	Phe	Val	Ser	Pro	Leu	Cys	Met	Ala	Val	Leu	Thr	Thr	
218	570					575				580							
220	GCC	AGC	ATC	ATC	CAG	CTG	GGG	GTC	ACG	CCC	CCG	GCC	TAC	AGC	GCC	TGG	2068
221	Ala	Ser	Ile	Ile	Gln	Leu	Gly	Val	Thr	Pro	Pro	Ala	Tyr	Ser	Ala	Trp	
222				590						595					600		
224	ATC	AAG	GAG	GAG	GCT	GCC	GAG	CGC	TAC	CTG	TAT	TTC	CCC	AAC	TGG	CCC	2116
225	Ile	Lys	Glu	Glu	Ala	Ala	Glu	Arg	Tyr	Leu	Tyr	Phe	Pro	Asn	Trp	Pro	
226			605						610					615			
228	ATG	GCA	CTC	CTG	ATC	ACC	CTC	ATC	GTC	GTG	GCG	ACG	CTG	CCC	ATC	CCT	2164
229	Met	Ala	Leu	Leu	Ile	Thr	Leu	Ile	Val	Val	Ala	Thr	Leu	Pro	Ile	Pro	
230			620					625					630				
232	GTG	GTG	TTC	GTC	CTG	CGG	CAC	TTC	CAC	CTG	CTC	TCT	GAT	GGC	TCC	AAC	2212
233	Val	Val	Phe	Val	Leu	Arg	His	Phe	His	Leu	Leu	Ser	Asp	Gly	Ser	Asn	
234		635					640					645					
236	ACC	CTC	TCC	GTG	TCC	TAC	AAG	AAG	GCC	CGC	ATG	ATG	AAG	GAC	ATC	TCC	2260
237	Thr	Leu	Ser	Val	Ser	Tyr	Lys	Lys	Ala	Arg	Met	Met	Lys	Asp	Ile	Ser	
238	650					655				660							
240	AAC	CTG	GAG	GAG	AAC	GAT	GAG	ACC	CGC	TTC	ATC	CTC	AGC	AAG	GTG	CCC	2308
241	Asn	Leu	Glu	Glu	Asn	Asp	Glu	Thr	Arg	Phe	Ile	Leu	Ser	Lys	Val	Pro	
242				670						675					680		
244	AGT	GAG	GCA	CCT	TCC	CCC	ATG	CCC	ACT	CAC	CGT	TCC	TAT	CTG	GGG	CCC	2356
245	Ser	Glu	Ala	Pro	Ser	Pro	Met	Pro	Thr	His	Arg	Ser	Tyr	Leu	Gly	Pro	
246			685						690					695			
248	GGC	AGC	ACA	TCA	CCC	CTG	GAG	ACC	AGC	TGG	AAC	CCC	AAT	GGA	CCC	TAT	2404
249	Gly	Ser	Thr	Ser	Pro	Leu	Glu	Thr	Ser	Trp	Asn	Pro	Asn	Gly	Pro	Tyr	
250			700					705					710				
252	GGG	CGC	GGC	TAC	CTG	CTG	GCC	AGC	ACC	CCT	GAG	TCT	GAG	CTG			2446
253	Gly	Arg	Gly	Tyr	Leu	Leu	Ala	Ser	Thr	Pro	Glu	Ser	Glu	Leu			
254		715					720						725				
256	TGACCACTGC	CCAAGCCCAT	GCCCGCTCTC	CCCCACCCG													2485
259	(2)	INFORMATION	FOR	SEQ	ID	NO:	2:										
261	(i)	SEQUENCE	CHARACTERISTICS:														
262	(A)	LENGTH:	727	amino	acids												
263	(B)	TYPE:	amino	acid													

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264      (D) TOPOLOGY: linear
266      (ii) MOLECULE TYPE: protein
268      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
270 Met Pro Lys Asn Ser Lys Val Thr Gln Arg Glu His Ser Ser Glu His
271 1      5      10      15
273 Val Thr Glu Ser Val Ala Asp Leu Leu Ala Leu Glu Glu Pro Val Asp
274      20      25      30
276 Tyr Lys Gln Ser Val Leu Asn Val Ala Gly Glu Ala Gly Gly Lys Gln
277      35      40      45
279 Lys Ala Val Glu Glu Glu Leu Asp Ala Glu Asp Arg Pro Ala Trp Asn
280      50      55      60
282 Ser Lys Leu Gln Tyr Ile Leu Ala Gln Ile Gly Phe Ser Val Gly Leu
283 65      70      75      80
285 Gly Asn Ile Trp Arg Phe Pro Tyr Leu Cys Gln Lys Asn Gly Gly Gly
286      85      90      95
288 Ala Tyr Leu Val Pro Tyr Leu Val Leu Leu Ile Ile Ile Gly Ile Pro
289      100      105      110
291 Leu Phe Phe Leu Glu Leu Ala Val Gly Gln Arg Ile Arg Arg Gly Ser
292      115      120      125
294 Ile Gly Val Trp His Tyr Ile Cys Pro Arg Leu Gly Gly Ile Gly Phe
295      130      135      140
297 Ser Ser Cys Ile Val Cys Leu Phe Val Gly Leu Tyr Tyr Asn Val Ile
298 145      150      155      160
300 Ile Gly Trp Ser Ile Phe Tyr Phe Phe Lys Ser Phe Gln Tyr Pro Leu
301      165      170      175
303 Pro Trp Ser Glu Cys Pro Val Val Arg Asn Gly Ser Val Ala Val Val
304      180      185      190
306 Glu Ala Glu Cys Glu Lys Ser Ser Ala Thr Thr Tyr Phe Trp Tyr Arg
307      195      200      205
309 Glu Ala Leu Asp Ile Ser Asp Ser Ile Ser Glu Ser Gly Gly Leu Asn
310      210      215      220
312 Trp Lys Met Thr Leu Cys Leu Leu Val Val Trp Ser Ile Gly Gly Met
313 225      230      235      240
315 Ala Val Gly Lys Gly Ile Gln Ser Ser Gly Lys Val Met Tyr Phe Ser
316      245      250      255
318 Ser Leu Phe Pro Tyr Val Val Leu Ala Cys Phe Leu Val Arg Gly Leu
319      260      265      270
321 Leu Leu Arg Gly Ala Val Asp Gly Ile Leu His Met Phe Thr Pro Lys
322      275      280      285
324 Leu Val Lys Met Leu Asp Pro Gln Val Trp Arg Glu Val Ala Thr Gln
325      290      295      300
327 Val Phe Phe Gly Leu Gly Leu Gly Phe Gly Gly Val Ile Val Phe Ser
328 305      310      315      320
330 Ser Tyr Asn Lys Gln Asp Asn Asn Cys His Phe Asp Gly Ala Leu Val
331      325      330      335
333 Ser Phe Ile Asn Phe Phe Thr Ser Val Leu Ala Thr Leu Val Val Phe
334      340      345      350
336 Val Val Leu Gly Phe Lys Ala Asn Ile Met Asn Glu Lys Cys Val Val
337      355      360      365

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09923444A.txt

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]